

UNITED STATES PATENT AND TRADEMARK OFFICE  
**CERTIFICATE OF CORRECTION**

PATENT NO. : 7,250,165 B2  
APPLICATION NO. : 09/920137  
DATED : July 31, 2007  
INVENTOR(S) : Heavner et al.

Page 1 of 27

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Column 73

Line 21, delete the entire sequence listing through column 84, line 19, and insert

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SEQUENCE LISTING

<210> 1

<211> 5

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<222> (1)..(5)

<223> Heavy Chain complementarity determinng region 1 (CDR1).

<400> 1

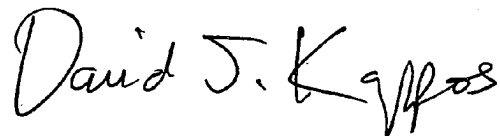
Ser Tyr Ala Met His

1

5

Signed and Sealed this

Tenth Day of August, 2010



David J. Kappos  
*Director of the United States Patent and Trademark Office*

<210> 2

<211> 17

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(17)

<223> Heavy Chain complementarity determinng region 2 (CDR2).

<220>

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<222> (1)..(1)

<223> Xaa at position 1 is selected from Ile, Phe or Val.

<220>

<221> MISC\_FEATURE

<222> (2)..(2)

<223> Xaa at position 2 is selected from Ile or Met.

<220>  
<221> MISC\_FEATURE  
<222> (3)..(3)  
<223> Xaa at position 3 is selected from Ser or Leu.

<220>  
<221> MISC\_FEATURE  
<222> (4)..(4)  
<223> Xaa at position 4 is selected from Tyr or Phe.

<220>  
<221> MISC\_FEATURE  
<222> (10)..(10)  
<223> Xaa at position 10 is selected from Lys or Tyr.

<220>  
<221> MISC\_FEATURE  
<222> (11)..(11)  
<223> Xaa at position 11 is selected from Ser or Tyr.

<220>

<221> MISC\_FEATURE

<222> (17)..(17)

<223> Xaa at position 17 is selected from Asp or Gly.

<400> 2

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Xaa | Xaa | Asp | Gly | Ser | Asn | Lys | Xaa | Xaa | Ala | Asp | Ser | Val | Lys | Xaa |
| 1   |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

<210> 3

<211> 17

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(17)

<223> Heavy Chain complementarity determinng region 3 (CDR3).

<220>  
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<222> (4) .. (4)  
<223> Xaa at position 4 is selected from Ile or Val.

<220>  
<221> MISC\_FEATURE  
<222> (5) .. (5)  
<223> Xaa at position 5 is selected from Ser, Ala or Gly.

<220>  
<221> MISC\_FEATURE  
<222> (9) .. (9)  
<223> Xaa at position 9 is selected from Asn or Tyr.

<400> 3

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Gly | Xaa | Xaa | Ala | Gly | Gly | Xaa | Tyr | Tyr | Tyr | Tyr | Gly | Met | Asp | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |

<210> 4

<211> 11

<212> PRT

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<222> (1)..(11)

<223> Light Chain complementarity determinng region 1 (CDR1).

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<222> (7)..(7)

<223> Xaa at position 7 is selected from Ser or Tyr.

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Arg Ala Ser Gln Ser Val Xaa Ser Tyr Leu Ala

1

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10

<210> 5

<211> 7

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<213> Homo sapiens

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<223> Light Chain complementarity determinng region 2 (CDR2).

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Asp Ala Ser Asn Arg Ala Thr

1

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<210> 6

<211> 10

<212> PRT

<213> Homo sapiens

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<222> (1)..(10)

<223> Light Chain complementarity determinng region 3 (CDR3).

<400> 6

Gln Gln Arg Ser Asn Trp Pro Pro Phe Thr

1 5 10



<210> 7

<211> 126

<212> PRT

<213> Homo sapiens

<400> 7

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1                      5                      10                      15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr

20                      25                      30

Ala Met His Trp Val Arg Gln Ala Pro Gly Asn Gly Leu Glu Trp Val

35                      40                      45

Ala Phe Met Ser Tyr Asp Gly Ser Asn Lys Lys Tyr Ala Asp Ser Val

50                      55                      60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr

65                      70                      75                      80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Asp Arg Gly Ile Ala Ala Gly Gly Asn Tyr Tyr Tyr Tyr Gly  
 100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
 115 120 125

<210> 8

<211> 108

<212> PRT

<213> Homo sapiens

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Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly  
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Tyr Ser Tyr  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
 35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro  
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro  
 85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys  
 100 105

<210> 9

<211> 157

<212> PRT

<213> Homo sapiens

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<221> MISC\_FEATURE

<222> (1)..(157)

<223> human TNF alpha monomer sequence

<400> 9

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Ser | Ser | Ser | Arg | Thr | Pro | Ser | Asp | Lys | Pro | Val | Ala | His | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Asn | Pro | Gln | Ala | Glu | Gly | Gln | Leu | Gln | Trp | Leu | Asn | Arg | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Ala | Leu | Leu | Ala | Asn | Gly | Val | Glu | Leu | Arg | Asp | Asn | Gln | Leu |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |

Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe  
50 55 60

Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile  
65 70 75 80

Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala  
85 90 95

Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys  
100 105 110

Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys  
115 120 125

Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe  
130 135 140

Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu  
145                      150                      155

<210> 10

<211> 18

<212> DNA

<213> Homo sapiens

<400> 10

ttggtccagt cggactgg 18

<210> 11

<211> 18

<212> DNA

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cacctgcact cggtgctt 18

<210> 12

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<400> 12

cactgttttg agtgtgtacg ggcttaagtt

30

<210> 13

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<212> DNA

<213> Homo sapiens

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gccgcacgtg tggaaggg

18

<210> 14

<211> 25

<212> DNA

<213> Homo sapiens

<400> 14

agtcaaggtc ggactggctt aagtt

25

<210> 15

<211> 28

<212> DNA

<213> Homo sapiens

<400> 15

gttgccccct ctcacaatct tcgaattt

28



<210> 16

<211> 18

<212> DNA

<213> Homo sapiens

<400> 16

ggcggtagac tactcgtc

18

<210> 17

<211> 7

<212> PRT

<213> Homo sapiens

<400> 17

Met Asp Trp Thr Trp Ser Ile

1

5

<210> 18

<211> 35

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<213> Homo sapiens

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tttcgtacgc caccatggac tggacctgga gcatc

35

<210> 19

<211> 34

<212> DNA

<213> Homo sapiens

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tttcgtacgc caccatgggg tttgggctga gctg

34

<210> 20

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<212> DNA

<213> Homo sapiens

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tttcgtacgc caccatggag ttggggctga gcatg 35

<210> 21

<211> 35

<212> DNA

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tttcgtacgc caccatgaaa cacctgtggt tcttc 35

<210> 22

<211> 35

<212> DNA

<213> Homo sapiens

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tttcgtacgc caccatgggg tcaaccgcca tcttc

35

<210> 23

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<213> Homo sapiens

<400> 23

Thr Val Thr Val Ser Ser

1

5

<210> 24

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<212> DNA

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gtgccagtgg cagaggagtc cattcaagct taagtt

36

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<211> 5

<212> PRT

<213> Homo sapiens

<400> 25

Met Asp Met Arg Val

1

5

<210> 26

<211> 31

<212> DNA

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tttgtcgaca ccatggacat gagggtcctc c

31

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<211> 28

<212> DNA

<213> Homo sapiens

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tttgtcgaca ccatggaagc cccagctc

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<210> 28

<211> 6

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Thr Lys Val Asp Ile Lys

1 5

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<400> 29

ctggtttcac ctatagtttg cattcagaat tcggcgctt t

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<210> 32

<211> 19

<212> PRT

<213> Homo sapiens

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<222> (1)..(19)

<223> Signal sequence for heavy chain variable region sequences as presented in original Figure 4

<400> 32

Met Gly Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly

1

5

10

15

Val Gln Cys



<210> 33

<211> 20

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<222> (1)..(20)

<223> Signal sequence for light chain variable region sequences as presented in original Figure 5

<400> 33

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro

1

5

10

15

Asp Thr Thr Gly

20

<210> 34

<211> 428

<212> DNA

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<222> (1)..(421)

<223> heavy chain variable region DNA sequences as presented in original Figure 2A-2B

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gtgcagctgg tggagtctgg gggaggcgtg gtccagcctg ggaggtccct gagactctcc 120
tgtgcagcct ctggttcacc ttcagtagct atgctatgca ctgggtccgc caggctccgg 180
caaggggctg gagtgggtgg cagttatata atatgatgga aaataaatac tacgcagact 240
ccgtgaaggg ccgattcacc atctagagac aattccaaga acacgctgta tctgcaaatg 300
aacagccaga gctgaggaca cggtgtgtga ttactgtgcg agagatcgag gtatatcagc 360
aggtggaata ctactactac tacggtatgg acgtctgggg gcaagggacc acggtcaccg 420
tctcctca                                         428
```

<210> 35

<211> 387

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(387)

<223> light chain variable region DNA sequences as presented in original Figure 3

<400> 35

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gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 120
ctctcctgca gggccagtea gagtgttagc agctacttag cctggtacca acagaaacct 180
ggccaggctc ccaggtcct catctatgat gcatccaaca gggccactgg catcccagcc 240
aggttcagtg gcagtgggtc tgggacagac ttactctca ccatcagcag cctagagcct 300
gaagattttg cagtttatta ctgtcagcag cgtagcaact ggcctccatt cactttcggc 360
cctgggacca aagtggatat caaacgt                                     387
```

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